

SEQUENCE SUBMISSION

SEQ ID NO: 1 is a primate HDTEA84 nucleic acid sequence.
SEQ ID NO: 2 is a primate HDTEA84 amino acid sequence.
5 SEQ ID NO: 3 is a primate HSLJD37R nucleic acid sequence.
SEQ ID NO: 4 is a primate HSLJD37R amino acid sequence.
SEQ ID NO: 5 is supplemented primate HSLJD37R nucleic acid sequence.
SEQ ID NO: 6 is supplemented primate HSLJD37R amino acid sequence.
SEQ ID NO: 7 is variant primate HSLJD37R nucleic acid sequence.
10 SEQ ID NO: 8 is variant primate HSLJD37R amino acid sequence.
SEQ ID NO: 9 is murine TNF-R2 amino acid sequence.
SEQ ID NO: 10 is human TNF-R2 amino acid sequence.
SEQ ID NO: 11 is human OPG amino acid sequence.
SEQ ID NO: 12 is a rodent RANKL nucleic acid sequence.
15 SEQ ID NO: 13 is a rodent RANKL amino acid sequence.
SEQ ID NO: 14 is a primate RANKL nucleic acid sequence.
SEQ ID NO: 15 is a primate RANKL amino acid sequence.
SEQ ID NO: 16 is another primate RANKL nucleic acid sequence.
SEQ ID NO: 17 is another primate RANKL amino acid sequence.
20 SEQ ID NO: 18 is a variant primate RANKL nucleic acid sequence.
SEQ ID NO: 19 is a variant primate RANKL amino acid sequence.

<110> Murphy, Erin E.
Mattson, Jeanine D.
25 Bates, Elizabeth Esther Mary
Gorman, Daniel M.
Lebecque, Serge J.E.

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	Thr Asn Thr Ser Leu Arg Val Cys Ser Ser Cys Pro Val Gly Thr Phe	
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	Thr Arg His Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro	
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55	His	Trp	Lys	Ala	Ala	Arg	Thr	Lys	Asp	Gly	Ile	Pro	Trp	His	Lys	Xaa	
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 1 5 10
 25 tgg gga cgg tgt gtc acc tgc caa cgg tgt ggt cct gga cag gag cta 158
 Trp Gly Arg Cys Val Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu
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 30 tcc aag gat tgt ggt tat gga gag ggt gga gat gcc tac tgc aca gcc 206
 Ser Lys Asp Cys Gly Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala
 30 35 40
 35 tgc cct cct cgc agg tac aaa agc agc tgg ggc cac cac aaa tgt cag 254
 Cys Pro Pro Arg Arg Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln
 45 50 55
 40 agt tgc atc acc tgt gct gtc atc aat cgt gtt cag aag gtc caa ctg 302
 Ser Cys Ile Thr Cys Ala Val Ile Asn Arg Val Gln Lys Val Gln Leu
 60 65 70 75
 cac agc taacctctna tgctgtctgt ggggatgttt gncccaagtt ctnaccgaaa 358
 His Ser
 45 agacacgccca tgggaaggct ggcaggacca ngaatggccn tcccgtggca gaaagccaga 418
 ccccccaacn nctgnagggt ccaatgtggc cttncattt ggaagcttan tgggaaggca 478
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 Trp Gly Arg Cys Val Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu
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 Ser Lys Asp Cys Gly Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala
 30 35 , 40
 45
 tgc cct cct cgc agg tac aaa agc agc tgg ggc cac cac aaa tgt cag 254
 Cys Pro Pro Arg Arg Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln
 45 50 55
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 Ser Cys Ile Thr Cys Ala Val Ile Asn Arg Val Gln Lys Val Asn Cys
 60 65 70 75
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 aca gct acc tct aat gct gtc tgt ggg gac tgt ttg ccc agg ttc tac 350
 Thr Ala Thr Ser Asn Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr
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 cga aag aca cgc att gga ggc ctg cag gac caa gag tgc atc ccg tgc 398
 Arg Lys Thr Arg Ile Gly Gly Leu Gln Asp Gln Glu Cys Ile Pro Cys
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	Leu Val Glu Ala Asp Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu	
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	Val Ala Leu Val Ser Ser Leu Leu Val Val Phe Thr Leu Ala Phe Leu	
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	Gly Leu Phe Phe Leu Tyr Cys Lys Gln Phe Phe Asn Arg His Cys Gln	
	160 165 170	
	cgt gga ggt ttg ctg cag ttt gag gct gat aaa aca gca aag gag gaa	638
	Arg Gly Gly Leu Leu Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu	
	175 180 185	
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	Ser Leu Phe Pro Val Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln	
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	Val Ser Trp Ala Pro Gly Ser Leu Ala Gln Leu Phe Ser Leu Asp Ser	
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	35 40 45	
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	50 55 60	
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Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr Arg Lys Thr Arg Ile
85 90 95

5 Gly Gly Leu Gln Asp Gln Glu Cys Ile Pro Cys Thr Lys Gln Thr Pro
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Thr Ser Glu Val Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp
115 120 125

10 Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Val Ser
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Ser Leu Leu Val Val Phe Thr Leu Ala Phe Leu Gly Leu Phe Phe Leu
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15 Tyr Cys Lys Gln Phe Phe Asn Arg His Cys Gln Arg Gly Gly Leu Leu
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20 Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe Pro Val
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Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Val Ser Trp Ala Pro
195 200 205

25 Gly Ser Leu Ala Gln Leu Phe Ser Leu Asp Ser Val Pro Ile Pro Gln
210 215 220

Gln Gln Gln Gly Pro Glu Met
225 230

30